

WOUTER MEULEMAN

Altius Institute for Biomedical Sciences
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Computational Biologist with independent NIH funding (R35 \$300k direct/year) and high-impact well-cited papers, including corresponding authorship (Nature, 2020). Research interests on the interface of large-scale (epi)genomic data analysis, machine learning and visualization. Particular interest in the functional organization of the regulatory genome.

RESEARCH EXPERIENCE

2016-: Independent Investigator, Head of Cell Systems Lab

Altius Institute for Biomedical Sciences, Seattle, WA USA

- **Leadership responsibilities:**

Core institute leadership and founding faculty member.

Mentoring and supervising 10+ FTEs (4 PhDs) in computational and experimental sciences.

- **Research program in the functional organization of the human regulatory genome:**

- Large-scale integrative data analysis, summarization and visualization.
- Developed methods for the delineation of regulatory elements in the human and mouse genomes.
- Established a novel component-based annotation of the regulatory genome.
- Annotated the regulatory landscapes of genes, pathways and disease-associated genetic variation.

- **Additional research and collaborations:**

- Set up internal initiative for Machine Learning approaches in Biology, incl. hiring PhD-level computational researchers and coordinating the setup of computational infrastructure.
- Design and validation of synthetic cell-type selective regulatory sequences using machine learning.
- Development of integrative genomic data visualizations, in collaboration with Harvard University.
- Predictive modeling of transcription start events in the human and fly genome, in collaboration with Oregon State University.

2012-6: Postdoctoral Associate in Computational Biology

Massachusetts Institute of Technology & Broad Institute of MIT and Harvard, Cambridge, MA USA

- **Advisor:** Prof. Manolis Kellis, MIT

- **NIH Roadmap Epigenomics Project:**

Lead scientist and data coordinator for the integrative analysis as part of the NIH Common Fund's Epigenomics Program. Constructed the then-largest epigenomic and regulatory reference maps, now used to study epigenomic variation, gene regulation and interpretation of genetic variants.

- **Additional research and collaborations:**

- Developed a novel information theory based method for the analysis of chromatin state data and collaborated with Washington University on the visualization of such data.
- Led the analysis of combinatorial binding patterns of chromatin regulator proteins, in collaboration with Massachusetts General Hospital.
- Discovered higher-order epigenomic patterns by building multi-scale chromatin state models, in collaboration with Dana Farber Cancer Institute and Harvard Medical School.
- Constructed descriptive and predictive models of higher-order genome organization.

- **Student supervision and teaching:**

Supervised 15+ students at undergraduate, Master and PhD levels, during thesis, rotation and class projects. Taught classes on three-dimensional genome organization to undergraduate and graduate MIT students.

EDUCATION

2012: PhD in Computational Biology

Netherlands Cancer Institute & Delft University of Technology, the Netherlands

- **Thesis:** *Computational Biology in Clinical Proteomics and Chromatin Genomics*
- **Advisors:** Prof. Bas van Steensel, Prof. Marcel Reinders & Prof. Lodewyk Wessels
- **Research:**
 - Co-discovered and characterized Lamina Associated Domains (LADs) in human and mouse. Analyzed dynamics of LADs during stem cell differentiation, performed comparative studies between human and mouse, and developed models for predicting LADs from DNA sequence features.
 - Developed methods for the analysis of mass spectrometry data, including a systematic comparison of normalization methods and an improved method for peak detection and quantification.

2005: M.Sc in Computer Science, minor in Molecular Biology, Leiden University, the Netherlands

- **Thesis:** *Integration and analysis of zebrafish microarray data*
- M.Sc thesis work performed at the Sanger Institute, Hinxton, and Brunel University, London, UK.

2002: B.Sc in Computer Science, The Hague University, the Netherlands

- **Thesis:** *Application of high-speed Linux clusters to bioinformatics problems*
- B.Sc thesis work performed at the University of Cambridge, UK. Awarded 10 out of 10.

INVITED TALKS

2020 Mathematical Frameworks for Integrative Analysis of Emerging Biological Data Types (BIRS, virtual)

2019 Pacific Symposium on Biocomputing, Big Island of Hawai'i, HI

2018 "Chromatin, Epigenetics and Gene Expression course", CSHL, Cold Spring Harbor, NY

2018 Panels on career development, ENCODE Consortium meeting, Palo Alto, CA

2016 Ludwig Maximilian University, Munich, Germany

2016 Utrecht University, Utrecht, the Netherlands

2016 Vertex Pharmaceuticals, Boston, MA

2016 f-Tales "Light on the dark side of the genome", keynote and workshop, Ghent, Belgium

2016 Roadmap Epigenomics Workshop, Epigenomics 2016, Puerto Rico

2015 International Human Epigenome Consortium annual meeting, Tokyo, Japan

2015 BroadE Workshop: Strategies for Visualizing Data, Broad Institute, Cambridge, MA

2015 UMASS Medical School, Worcester, MA

2015 Roadmap Epigenomics Workshop, Keystone meeting on Epigenomics, Keystone, CO

2015 Panel on Data Sharing and Standardization, Festival of Genomics, Boston, MA

2013 Delft University of Technology, Delft, the Netherlands

2013 Translating Epigenomes into Function: a Next Generation Challenge for Human Disease, Capri, Italy

2011 Massachusetts Institute of Technology, Cambridge, MA

2011 UMASS Medical School, Worcester, MA

2011 Harvard University, Boston, MA

2011 Columbia University, New York, NY

2010 Utrecht University, Utrecht, the Netherlands

2009 Radboud University Nijmegen Medical Centre, Nijmegen, the Netherlands

2006 Clinical proteomics symposium, Utrecht, the Netherlands

HONORS and AWARDS

- 2020 Genomic Innovator Award**, regarding the elucidation of the organizing principles of the regulatory genome through large-scale data integration (NIH R35 HG011317-01, \$300k direct/year)
- 2015** Best talk prize at International Human Epigenome Consortium annual meeting, Tokyo, Japan
- 2015** Best poster prize at Broad Institute CBBO retreat, Cambridge, MA
- 2014** Contributed to a successfully funded R01 grant regarding the post-GWAS interpretation of genetic variants using epigenomic reference maps (HG008155-01, \$499k direct/year)
- 2014** Co-wrote a successfully funded R01 grant regarding epigenomic comparison and clustering, predicting the three-dimensional genome organization and gene-enhancer linking (GM113708-01, \$250k direct/year).
- 2014** Best poster prize at Broad Institute retreat, Boston, MA
- 2011** Best poster prize at Netherlands Bioinformatics Centre (NBIC) conference
- 2010** EMBO Short Term Fellowship to visit lab of Manolis Kellis at MIT
- 2010** Best poster prize at ISMB student council conference, Boston, MA
- 2003-** Various fellowships for attending (inter)national conferences

TEACHING EXPERIENCE

- 2018 Guest lecturer**, Cold Spring Harbor Laboratory
Course: "Chromatin, Epigenetics and Gene Expression"
Provided an interactive two-hour lecture on genome organization, chromatin states and gene regulation.
- 2012-6 Guest lecturer**, Massachusetts Institute of Technology
Course: "Computational Biology: Genomes, Networks, Evolution" (6.047/6.878/HST.507)
Lectured on the three-dimensional organization of the human genome to a class of 50 MIT students.
- 2015 Lecturer**, Massachusetts Institute of Technology
Taught a class on the cellular organization of DNA to a group of 70 middle school students, as part of MIT's Educational Studies Program (ESP).
- 2010-1 Guest lecturer**, Delft University of Technology
Course: "Genome-scale data analysis"
Lectured on clinical biomarker discovery using mass spectrometry and machine learning, and three-dimensional organization of the human genome, to classes of 30 graduate students.
- 2010-1 Course co-designer and instructor**, Netherlands Cancer Institute
Course: "R and statistics for Biologists"
Developed and led hands-on training to wet-lab biologists concerning data pre-processing, differential gene expression analysis, transcription factor binding site analysis and gene set enrichment.
- 2005-9 Member of five M.Sc thesis committees**, Delft University of Technology
- 2008 Instructor**, Delft University of Technology
Course: "Bioinformatics", as part of the ASCI graduate school curriculum
Responsible for the design and instruction of the lab section dealing with sequence analysis and transcription factor binding site discovery.
- 2004 Teaching Assistant**, Leiden University
Course: "Computer architecture", as part of the core Computer Science curriculum.
Responsible for leading and grading lab practicals regarding the design and implementation of central processing unit (CPU) simulators.
- 2003-4 Member of Curriculum Committee**, Leiden University

PROFESSIONAL SERVICE

- Organizing committee of the ENCODE Users meeting, Stanford University, 2016.
- Reviewer for: Nature Structural and Molecular Biology, Nature Scientific Reports, Nature Communications, Molecular Systems Biology, Proteomics, Chromosome Research, RECOMB conference, BMC Biology, BMC Bioinformatics, BMC Microbiology, Cancer informatics, ISMB conference, PeerJ.

PUBLICATIONS

- W. Meuleman[†], A. Muratov, E. Rynes, J. Halow, K. Lee, D. Bates, M. Diegel, D. Dunn, J. Neri, A. Teodosiadis, A. Reynolds, E. Haugen, J.S. Nelson, A. Johnson, M. Frerker, M. Buckley, R. Sandstrom, J. Vierstra, R. Kaul, J.A. Stamatoyannopoulos[†] – Index and biological spectrum of human DNase I hypersensitive sites, **NATURE**, Vol. 584, pp. 244–251 (2020).
- J. Vierstra, J. Lazar, R., J. Halow, K. Lee, D. Bates, M. Diegel, D. Dunn, F. Neri, E. Haugen, E. Rynes, A. Reynolds, J. Nelson, A. Johnson, M. Frerker, M. Buckley, R. Kaul, W. Meuleman, J.A. Stamatoyannopoulos – Global reference mapping of human transcription factor footprints, **NATURE**, Vol. 583, pp. 729–736 (2020).
- C.E. Breeze, J. Lazar, T. Mercer, J. Halow, I. Washington, K. Lee, S. Ibarrientos, A. Castillo, F. Neri, E. Haugen, E. Rynes, A. Reynolds, D. Bates, M. Diegel, D. Dunn, R. Kaul, R. Sandstrom, W. Meuleman, M.A. Bender, M. Groudine, J.A. Stamatoyannopoulos – Atlas and developmental dynamics of mouse DNase I hypersensitive sites, **bioRxiv**, 2020
- C.B. Adsera, Y. Park, W. Meuleman, M. Kellis – Integrative analysis of 10,000 epigenomic maps across 800 samples for regulatory genomics and disease dissection, **bioRxiv**, 2019
- H.J.G. van de Werken, J.C. Haan, Y. Feodorova, D. Bijos, A. Weuts, K. Theunis, S.J.B. Holwerda, W. Meuleman, L. Pagie, K. Thanisch, P. Kumar, H. Leonhardt, P. Marynen, B. van Steensel, T. Voet, W. de Laat, I. Solovei, B. Joffe – Small chromosomal regions position themselves autonomously according to their chromatin class, **Genome Research**, Vol. 27 No. 6, pp. 922–933 (2017).
- E. Marco*, W. Meuleman*, J. Huang*, K. Glass, L. Pinello, J. Wang, M. Kellis, G.C. Yuan – Multi-scale chromatin state annotation using a hierarchical hidden Markov model, **Nature communications**, Vol. 8, No. 15011 (2017).
- H.J.G. van de Werken, J.C. de Haan, Y. Feodorova, D. Bijos, A. Weuts, K. Theunis, S. Holwerda, W. Meuleman, L. Pagie, K. Thanisch, P. Kumar, H. Leonhardt, P. Marynen, B. van Steensel, T. Voet, W. de Laat, I. Solovei, B. Joffe – Small chromosomal regions position themselves autonomously according to their chromatin class, **Genome Research**, Vol. 27, pp. 922–933 (2017).
- A. Kundaje*, W. Meuleman*, J. Ernst*, M. Bilenky*, *et al.* (248 authors) – Integrative analysis of 111 reference human epigenomes, **NATURE**, Vol. 518, No. 7539, pp. 317–330 (2015). **3300+ citations.**
- M. Claussnitzer, S.N. Dankel, K-H. Kim, G. Quon, W. Meuleman, C. Haugen, V. Glunk, I.S. Sousa, J.L. Beaudry, V. Puviindran, N.A. Abdennur, J. Liu, P-A. Svensson, Y-H. Hsu, D.J. Drucker, G. Mellgren, C-C. Hui, H. Hauner, M. Kellis – FTO obesity variant circuitry and adipocyte browning in humans, **New England Journal of Medicine**, Vol. 373, No. 10 (2015). **800+ citations.**
- R.A.H. van de Ven, M. Tenhagen*, W. Meuleman*, J.J.G. van Riel, R.C.J. Schackmann, P.W.B. Derksen – Nuclear p120-catenin regulates the anoikis resistance of mouse lobular breast cancer cells through Kaiso-dependent Wnt11 expression, **Disease models & mechanisms**, Vol. 8, No. 4 (2015).
- W. Akhtar, J. de Jong, A.V. Pindyurin, L. Pagie, W. Meuleman, J. de Ridder, A. Berns, L.F.A. Wessels, M. van Lohuizen, B. van Steensel – Chromatin position effects assayed by thousands of reporters integrated in parallel, **CELL**, Vol. 154, No. 4 (2013). **200+ citations**

- W. Meuleman^{*}, D. Peric-Hupkes^{*}, J. Kind, J.B. Beaudry, L. Pagie, M. Kellis, M.J.T. Reinders, L.F.A. Wessels, B. van Steensel – Constitutive nuclear lamina-genome interactions are highly conserved and associated with A/T-rich sequence, **Genome Research**, Vol. 23, No. 2, pp. 270–280 (2013). **300+ citations**.
- W. Meuleman, Computational Biology in Clinical Proteomics and Chromatin Genomics – PhD thesis (2012).
- N. Kubben, M. Adriaens, W. Meuleman, J.W. Voncken, B. van Steensel, T. Misteli – Mapping of lamin A-and progerin-interacting genome regions, **Chromosoma**, Vol. 121, No. 5 (2012).
- D. Peric-Hupkes^{*}, W. Meuleman^{*}, L. Pagie, S. Bruggeman, I. Solovei, W. Brugman, S. Gräf, P. Flicek, R. Kerkhoven, M. van Lohuizen, M.J.T. Reinders, L.F.A. Wessels, B. van Steensel – Molecular maps of the reorganization of genome – nuclear lamina interactions during differentiation, **Molecular Cell**, Vol. 38, No. 4, pp. 603–613 (2010). **800+ citations**.
- J. van Bemmelen, L. Pagie, U. Braunschweig, W. Brugman, W. Meuleman, R. Kerkhoven, B. van Steensel – The insulator protein SU(HW) fine-tunes nuclear lamina interactions of the *Drosophila* genome, **PLoS One**, Vol. 5, No. 11, pp. e15013 (2010).
- W. Meuleman, J.Y.M.N. Engwegen, M.C. Gast, L.F.A. Wessels, M.J.T. Reinders – Analysis of mass spectrometry data using sub-spectra, **BMC Bioinformatics**, Vol. 10 Suppl 1, No. S51 (2009).
- L. Guelen, L. Pagie, E. Brasset, W. Meuleman, M.B. Faza, W. Talhout, B.H. Eussen, A. de Klein, L.F.A. Wessels, W. de Laat, B. van Steensel – Domain organization of human chromosomes revealed by mapping of nuclear lamina interactions, **NATURE**, Vol. 453, pp. 948–951 (2008). **1500+ citations**.
- W. Meuleman, J.Y.M.N. Engwegen, M.C. Gast, J.H. Beijnen, M.J.T. Reinders, L.F.A. Wessels – Comparison of normalisation methods for surface-enhanced laser desorption and ionisation (SELDI) time-of-flight (TOF) mass spectrometry data, **BMC Bioinformatics**, Vol. 9, No. 88 (2008).
- M. van Uitert, W. Meuleman, L.F.A. Wessels – Biclustering Sparse Binary Genomic Data, **Journal of Computational Biology**, Vol. 15, pp. 1329–1345 (2008).
- J.Y.M.N. Engwegen, A.C.T.M. Depla, M.E. Smits, A. Cats, H. Tuynman, H.A. van Heukelem, P. Snel, W. Meuleman, L.F.A. Wessels, J.H.M. Schellens, J.H. Beijnen – Detection of colorectal cancer by serum and tissue protein profiling: a prospective study in a population at risk, **Biomarker insights**, Vol. 3 (2008).
- W. Meuleman, M. Welten, F. Verbeek – Construction of correlation networks with explicit time-slices using time-lagged, variable interval standard and partial correlation coefficients, Computational Life Sciences II: Second International Symposium CompLife 2006, Cambridge (UK), **Lecture Notes in Bioinformatics**, Vol. 4216, pp. 236–246 (2006).

^{*}: equal contributions

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